

OIPE

11/2

RAW SEQUENCE LISTING
 PATENT APPLICATION: US/09/630,931

DATE: 08/16/2000
 TIME: 12:58:59

Input Set : A:\elitra6A.txt
 Output Set : N:\CRF3\08162000\I630931.raw

Does Not Comply
 Corrected Diskette Needed

4 <110> APPLICANT: Zyskind, Judith W.
 6 <120> TITLE OF INVENTION: CHITOBIASE AS A REPORTER ENZYME
 8 <130> FILE REFERENCE: ELITRA.006A
 C--> 10 <140> CURRENT APPLICATION NUMBER: US/09/630,931
 C--> 10 <141> CURRENT FILING DATE: 2000-08-02
 10 <150> PRIOR APPLICATION NUMBER: 60/159,221
 12 <151> PRIOR FILING DATE: 1999-10-13
 14 <160> NUMBER OF SEQ ID NOS: 19
 16 <170> SOFTWARE: FastSEQ for Windows Version 4.0

ERRORED SEQUENCES

861 <210> SEQ ID NO: 19
 862 <211> LENGTH: 880
 863 <212> TYPE: PRT
 864 <213> ORGANISM: Artificial Sequence
 866 <220> FEATURE:
 867 <223> OTHER INFORMATION: dnaA/Chitobiase Fusion
 869 <400> SEQUENCE: 19
 870 Met Ser Leu Ser Leu Trp Gln Gln Cys Leu Ala Arg Leu Gln Asp Glu
 871 1 5 10 15
 872 Leu Val Pro Ser Ser Glu Gln Gln Val Val Asn Ser Leu Ala Asp Asn
 873 20 25 30
 874 Leu Asp Ile Gln Tyr Glu Val Leu Thr Asn His Gly Ala Asn Glu Gly
 875 35 40 45
 876 Leu Ala Cys Gln Asp Met Gly Ala Glu Trp Ala Ser Cys Asn Lys Val
 877 50 55 60
 878 Asn Met Thr Leu Val Asn Gln Gly Glu Ala Val Asp Ser Lys Asp Trp
 879 65 70 75 80
 880 Ala Ile Tyr Phe His Ser Ile Arg Leu Ile Leu Asp Val Asp Asn Glu
 881 85 90 95
 882 Gln Phe Lys Ile Ser Arg Val Thr Gly Asp Leu His Lys Leu Glu Pro
 883 100 105 110
 884 Thr Asp Lys Phe Asp Gly Phe Ala Ala Gly Glu Glu Val Val Leu Pro
 885 115 120 125
 886 Leu Val Gly Glu Tyr Trp Gln Leu Phe Glu Thr Asp Phe Met Pro Gly
 887 130 135 140
 888 Ala Phe Val Ser Ala Pro Asn Ala Glu Pro Lys Met Ile Ala Ser Leu
 889 145 150 155 160
 890 Asn Thr Glu Asp Val Ala Ser Phe Val Thr Gly Leu Glu Gly Asn Asn
 891 165 170 175
 892 Leu Lys Arg Thr Pro Asp Asp Asn Asn Val Phe Ala Asn Ala Val Ser
 893 180 185 190
 894 Arg Phe Glu Lys Asn Glu Asp Leu Ala Thr Gln Asp Val Ser Thr Thr
 895 195 200 205
 896 Leu Leu Pro Thr Pro Met His Val Glu Ala Gly Lys Gly Lys Val Asp

see
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897 210 215 220
898 Ile Ala Asp Gly Ile Ala Leu Pro Lys Asp Ala Phe Asp Ala Thr Gln
899 225 230 235 240
900 Phe Ala Ala Ile Gln Asp Arg Ala Glu Val Val Gly Val Asp Val Arg
901 245 250 255
902 Gly Asp Leu Pro Val Ser Ile Thr Val Val Pro Ala Asp Phe Thr Gly
903 260 265 270
904 Glu Leu Ala Lys Ser Gly Ala Tyr Glu Met Ser Ile Lys Gly Asp Gly
905 275 280 285
906 Ile Val Ile Lys Ala Phe Asp Gln Ala Gly Ala Phe Tyr Ala Val Gln
907 290 295 300
908 Ser Ile Phe Gly Leu Val Asp Ser Gln Asn Ala Asp Ser Leu Pro Gln
909 305 310 315 320
910 Leu Ser Ile Lys Asp Ala Pro Arg Phe Asp Tyr Arg Gly Val Met Val
911 325 330 335
912 Asp Val Ala Arg Asn Phe His Ser Lys Asp Ala Ile Leu Ala Thr Leu
913 340 345 350
914 Asp Gln Met Ala Ala Tyr Lys Met Asn Lys Leu His Leu Thr
915 355 360 365
916 Asp Asp Glu Gly Trp Arg Leu Glu Ile Pro Gly Leu Pro Glu Leu Thr
917 370 375 380
918 Glu Val Gly Ala Asn Arg Cys Phe Asp Thr Gln Glu Lys Ser Cys Leu
919 385 390 395 400
920 Leu Pro Gln Leu Gly Ser Gly Pro Thr Thr Asp Asn Phe Gly Ser Gly
921 405 410 415
922 Tyr Phe Ser Lys Ala Asp Tyr Val Glu Ile Leu Lys Tyr Ala Lys Ala
923 420 425 430
924 Arg Asn Ile Glu Val Ile Pro Glu Ile Asp Met Pro Ala His Ala Arg
925 435 440 445
926 Ala Ala Val Val Ser Met Glu Ala Arg Tyr Asp Arg Leu Met Glu Glu
927 450 455 460
928 Gly Lys Glu Ala Glu Ala Asn Glu Tyr Arg Leu Met Asp Pro Gln Asp
929 465 470 475 480
930 Thr Ser Asn Val Thr Thr Val Gln Phe Tyr Asn Lys Gln Ser Phe Ile
931 485 490 495
932 Asn Pro Cys Met Glu Ser Ser Thr Arg Phe Val Asp Lys Val Ile Ser
933 500 505 510
934 Glu Val Ala Ala Met His Gln Glu Ala Gly Ala Pro Leu Thr Thr Trp
935 515 520 525
936 His Phe Gly Gly Asp Glu Ala Lys Asn Ile Lys Leu Gly Ala Gly Phe
937 530 535 540
938 Gln Asp Val Asn Ala Glu Asp Lys Val Ser Trp Lys Gly Thr Ile Asp
939 545 550 555 560
940 Leu Ser Lys Gln Asp Lys Pro Phe Ala Gln Ser Pro Gln Cys Gln Thr
941 565 570 575
942 Leu Ile Thr Asp Gly Thr Val Ser Asp Phe Ala His Leu Pro Ser His
943 580 585 590
944 Phe Ala Glu Glu Val Ser Lys Ile Val Ala Glu Lys Gly Ile Pro Asn
945 595 600 605

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946 Phe Gln Ala Trp Gln Asp Gly Leu Lys Tyr Ser Asp Gly Glu Lys Ala
947 610 615 620
948 Phe Ala Thr Glu Asn Thr Arg Val Asn Phe Trp Asp Val Leu Tyr Trp
949 625 630 635 640
950 Gly Gly Thr Ser Ser Val Tyr Glu Trp Ser Lys Lys Gly Tyr Asp Val
951 645 650 655
952 Ile Val Ser Asn Pro Asp Tyr Val Tyr Met Asp Met Pro Tyr Glu Val
953 660 665 670
954 Asp Pro Lys Glu Arg Gly Tyr Tyr Trp Ala Thr Arg Ala Thr Asp Thr
955 675 680 685
956 Arg Lys Met Phe Gly Phe Ala Pro Glu Asn Met Pro Gln Asn Ala Glu
957 690 695 700
958 Thr Ser Val Asp Arg Asp Gly Asn Gly Phe Thr Gly Lys Gly Glu Ile
959 705 710 715 720
960 Glu Ala Lys Pro Phe Tyr Gly Leu Ser Ala Gln Leu Trp Ser Glu Thr
961 725 730 735
962 Val Arg Asn Asp Glu Gln Tyr Glu Tyr Met Val Phe Pro Arg Val Leu
963 740 745 750
964 Ala Ala Ala Gln Arg Ala Trp His Arg Ala Asp Trp Glu Asn Asp Tyr
965 755 760 765
966 Lys Val Gly Val Glu Tyr Ser Gln Asn Ser Asn Leu Val Asp Lys Ala
967 770 775 780
968 Ser Leu Asn Gln Asp Tyr Asn Arg Phe Ala Asn Val Leu Gly Gln Arg
969 785 790 795 800
970 Glu Leu Ala Lys Leu Glu Lys Ser Gly Ile Asp Tyr Arg Leu Pro Val
971 805 810 815
972 Pro Gly Ala Lys Val Glu Asp Gly Lys Leu Ala Met Asn Val Gln Phe
973 820 825 830
974 Pro Gly Val Thr Leu Gln Tyr Ser Leu Asp Gly Glu Asn Trp Leu Thr
975 835 840 845
976 Tyr Ala Asp Asn Ala Arg Pro Asn Val Thr Gly Glu Val Phe Ile Arg
977 850 855 860
978 Ser Val Ser Ala Thr Gly Glu Lys Val Ser Arg Ile Thr Ser Val Lys
979 865 870 875 880
E--> 981 18
E--> 984 1

delete at end of file

see next page for more errors

<210> 15
 <211> 238
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> LacZ(/chitobiase Fusion

<220>
 <221> CDS
 <222> (119)...(240)

238 ← only 238 nucleotides in sequence 15

<221> -35 signal
 <222> (44)...(50)
 <223> Lac promoter

<221> -10 signal
 <222> (69)...(74)
 <223> Lac promoter
 <221> protein_bind
 <222> (81)...(107)
 <223> Lac repressor binding site

<221> protein bind
 <222> (7)...(34)
 <223> CAP-cAMP binding site

<400> 15
 gcatgcatta atgtgagtta gctcactcat taggcacccc aggctttaca ctttatgctt 60
 ccggctcgta tgttgtgtgg aattgtgagc ggataacaat ttcacacagg aaacagct 118
 atg acc atg att acg cca agc ttg cat gcc tgc agg tcg act cta gag 166
 Met Thr Met Ile Thr Pro Ser Leu His Ala Cys Arg Ser Thr Leu Glu
 1 5 10 15

gat ccc cgg gta ccg agc tct gag caa caa gtt gta aac tca ctg gct 214
 Asp Pro Arg Val Pro Ser Ser Glu Gln Gln Val Val Asn Ser Leu Ala
 20 25 30

gat aac ctt gat atc caa tat gaa 238
 Asp Asn Leu Asp Ile Gln Tyr Glu
 35 40

VERIFICATION SUMMARY
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L:10 M:270 C: Current Application Number differs, Replaced Current Application No
L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:61 M:283 W: Missing Blank Line separator, <210> field identifier
L:346 M:283 W: Missing Blank Line separator, <210> field identifier
L:560 M:283 W: Missing Blank Line separator, <220> field identifier
L:565 M:351 W: Sequence data Name/Key Feature Out-of-Range, SEQ ID#:15, CDS LOCATION: (119)...(240)
L:602 M:283 W: Missing Blank Line separator, <220> field identifier
L:617 M:283 W: Missing Blank Line separator, <220> field identifier
L:981 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:19
M:332 Repeated in SeqNo=19